

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2001, 09:44:54 ; Search time 3626.83 Seconds
(without alignments)
11766.617 Million cell updates/sec

Title: US-09-784-340-1

Perfect score: 2759

Sequence: 1 caaccattgcagcatcagtglt.....ctgtcagccgttactgtagcg 2759

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_ba3.*
- 4: gb_in1.*
- 5: gb_in2.*
- 6: gb_in3.*
- 7: gb_om.*
- 8: gb_ov.*
- 9: gb_pat1.*
- 10: gb_pat2.*
- 11: gb_ph.*
- 12: gb_pl1.*
- 13: gb_pl2.*
- 14: gb_pl3.*
- 15: gb_pl4.*
- 16: em_ba1.*
- 17: em_ba2.*
- 18: em_fun.*
- 19: em_higo_hum.*
- 20: em_higo_inv.*
- 21: em_higo_rod.*
- 22: em_hig_hum1.*
- 23: em_hig_hum2.*
- 24: em_hig_hum3.*
- 25: em_hig_hum4.*
- 26: em_hig_hum5.*
- 27: em_hig_hum6.*
- 28: em_hig_hum7.*
- 29: em_hig_hum8.*
- 30: em_hig_inv1.*
- 31: em_hig_inv2.*
- 32: em_hig_other.*
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- 35: em_hum2.*
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- 37: em_hum4.*
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- 39: em_hum6.*
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- 42: em_om.*
- 43: em_or.*

- 44: em_ov.*
- 45: em_pat.*
- 46: em_ph.*
- 47: em_pl.*
- 48: em_ro.*
- 49: em_sts.*
- 50: em_sy.*
- 51: em_un.*
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- 53: gb_sts1.*
- 54: gb_sts2.*
- 55: gb_sts3.*
- 56: gb_sy.*
- 57: gb_un.*
- 58: gb_v11.*
- 59: gb_v12.*
- 60: gb_hgt1.*
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- 62: gb_hgt3.*
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- 65: gb_hgt6.*
- 66: gb_hgt7.*
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- 86: gb_pr2.*
- 87: gb_pr3.*
- 88: gb_pr4.*
- 89: gb_pr5.*
- 90: gb_pr6.*
- 91: gb_pr7.*
- 92: gb_pr8.*
- 93: gb_pr9.*
- 94: gb_ro1.*
- 95: gb_ro2.*
- 96: gb_in4.*
- 97: gb_pr10.*
- 98: em_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2130.6	77.2	2786	89 AK025587 Homo sapi
2	1038.8	37.7	2547	94 AF175221 Cavia por
3	994.8	36.1	212904	66 AC021146 Homo sapi
4	967.4	35.1	1650	9 AX040087 Sequence
5	952.4	34.5	138665	72 AC055794 Homo sapi
6	821.2	29.8	1766	93 HSA6054 Human sapi
7	782	28.3	2090	97 HSU08854 Human sapi
8	778.8	28.2	2114	89 AF180322 Homo sapi

9	775.6	28.1	2107	97	HSU59209	U59209 Homo sapien
10	767.6	27.8	2108	89	AF112112	AF112112 Macaca fa
11	766.2	27.8	2123	99	HSU06641	U06641 Human UDP g
12	766	27.6	2079	93	HSAR5162	AJ005162 Homo sapi
13	762.8	27.6	1584	94	AF184901	AF184901 Mus muscu
14	762.8	27.6	2097	88	AF064200	AF064200 Homo sapi
15	758	27.5	2091	88	AF081793	AF081793 Homo sapi
16	758	27.5	2091	87	HSU01793	U00317 Human mRNA
17	757.6	27.5	2075	88	AF072223	AF072223 Macaca fa
18	754.8	27.4	1722	88	AF016492	AF016492 Homo sapi
19	754.8	27.4	1855	97	U05428	U05428 Human 3,4-C
20	753.4	27.3	212904	66	AC021146	AC021146 Homo sapi
21	751	27.2	1753	88	AF016310	AF016310 Macaca fa
22	748.4	27.1	1668	89	AF094901	AF094901 Macaca fasc
23	745.2	27.1	1668	89	AF094901	AF094901 Macaca fasc
24	743	26.9	1831	95	FRUGTGENE	X57565 Rattus norv
25	738.8	26.8	1662	89	AF294902	AF294902 Macaca mu
26	736	26.7	1851	89	AF172722	AF172722 Homo sapi
27	734	26.6	1768	89	AF112113	AF112113 Macaca fa
28	732.6	26.6	2299	97	HSU072B10	X63359 H. sapiens U
29	731.8	26.5	1671	7	RABUGT2B	L01082 Oryctolagus
30	701.4	25.4	1832	7	RABUGT2B	L01081 Oryctolagus
31	693.4	25.1	1961	95	RATUDPCTP	M13506 Rat liver U
32	684.2	24.8	2897	7	RABUGT2BC	L01083 Oryctolagus
33	678.6	24.6	2818	7	OCU72742	U72742 Oryctolagus
34	675.6	24.5	1844	95	RNU06273	U06273 Rattus norv
35	662.6	24.0	1846	95	RNU06274	U06274 Rattus norv
36	655.6	23.8	2634	95	RATUDPCTP	J02589 Rat UDP glu
37	647.2	23.5	1858	94	RATUDPCTP	X06358 Mouse mRNA
38	644.4	23.4	1716	95	RATUDPCTP	Y00156 Rat mRNA fo
39	640.2	23.2	1819	95	RATUDPCTP	M11109 Rat UDP glu
40	633.6	23.0	1846	95	RATUDPCTP	X03478 Rat liver m
41	626	22.7	1858	95	RATUDPCTP	M3746 Rat UDP glu
42	598	21.7	1947	95	RNU27518	U27518 Rattus norv
43	587.8	21.3	1500	89	AF172724	AF172724 Homo sapi
44	438.6	15.9	138015	69	AC025488	AC025488 Homo sapi
45	438.6	15.9	169246	62	AC011254	AC011254 Homo sapi

ALIGNMENTS

RESULT 1
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 DEFINITION Homo sapiens cDNA: FLJ21934 fis, clone HEP04364.
 ACCESSION AK025587
 VERSION AK025587.1 GI:10438147
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (sites)
 Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
 Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
 Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
 NEDO human cDNA Sequencing project
 Unpublished (2000)
 2 (bases 1 to 2786)
 Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
 Shibahara,T., Tanaka,T. and Nakamura,Y.
 Direct Submission
 Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
 Sugano, Institute of Medical Science, University of Tokyo,
 Laboratory of Genome Structure Analysis, Human Genome Center,
 Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
 (E-mail:cdna@leims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 Fax:81-3-5449-5416)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing; Research Association for Biotechnology; cDNA library

FEATURES
 source construction, 5'- & 3'-end one pass sequencing; Department of
 Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).
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 GRPTLCTEIVGAEIWLIRTYWDFEPPQYQNEFVGGIHKPKATPKEMPVOS
 SGEIDIVFSLGSLFQNTVEERKATIASALQIPKVMYRKKKPSTLGANTRLDW
 IPONDILGHPKRTKRTITGNGNITVETATYHYGVYGVPIFGQDNLNIAHMAKGAVE
 INEKTMSEDILTRATRYITTSSTKENMARSRIHDDVPKPLDRAVWIEFVNRKRG
 AKHURSAHDLTWQHTSIDVIGFLCAVVAIFLETKFLFSCQKFNKTRIERE"
 BASE COUNT 919 a 463 c 496 g 908 t
 ORIGIN

CDS

Query Match 77.2%; Score 2130.6; DB 89; Length 2786;
 Best Local Similarity 96.0%; Pred. No. 0;
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 1 ATTGACTCCTCAAGCAAGCCCTGCTTAATGACTACAGCAAGCCCTGCTGAATTTGA 60
 262 gttgtccatctgcccagagcagagcagagaaataattttgtgactagctct 321
 61 GGTGTCCTATATGCCACAGCAGACAGACAGAAATATATTTGTTGACCTAGCTCT 120
 322 gaatgctctgcccagccttatcaactggcaatcagttataaataatgattttgt 381
 121 GAATGCTCTTGGCAGGCTTATCACTGCACTAGTATATAAATTAATGATTTTGT 180
 382 tgaataagaggaacttaaaatgatggtggaagctttatcacaatcagagccttat 441
 181 TGAATTAAGAGAACTTTAAATAATGATGTGAGAGCTTTATATCAATCAAGAGCTTAT 240
 442 gaagaagctacaagaaacacactacgaatgaatgcttatagacccttgattccctgtg 501
 241 GAAGAAGCTACAGCAAGCAAGCTTATCAATGATGATGATGATGATGATGATGATG 300
 502 agacactatgctggaagttgcttgcagccctttgtgctcacaactagaaattctgtagg 561
 301 AGACCTATGCTGAGTGTGCTTGCAGTCCCTTTGCTCACTATGAAATTTCTGTAGG 360
 562 aggaacaataggaagcgaagcgtgtggaactcagcctcaccattccattactatgccc 621
 361 AGGCAATATGAGCAGCAAGCTGTGGGAACCTTCAGCTCCACTTCTATATGCTGTGCC 420
 622 tatgacagagactacaagcagaatgacaccttcggaagaagataaaatcaatgcttcc 681
 421 TATGACAGGACTACAGCAGAAATGACCTTTCGGAAGAGTAAATAATTCATATGCTTTC 480
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 742 taagattataggaagcccaactacattatgagagctgtggaaaagcgtgagatatgct 801
 541 TAAAGCATTAGGAAGCCCACTACATTATGAGAGCTGTGGAAAAGCTGAGATATGCT 600

OY	802	atacagacatatttggatttlltgaatttctctcaacatataccaactaacttggatttgt	861
Db	601	AATACGAACATATTGGGATTTTGAATTTTCCCTCCACACATATCCAACTTAACCTTGGATTGGT	660
OY	862	tggagagatcgaactgaacactgcgaagacttgcctaagagaaatggaaaatttggcca	921
Db	661	TGGAGGATTGCACGTAAACCTGCGCAAGCTTTGGCTTAAGGAAATGGAAAATTTTGTCCA	720
OY	922	gaatcaggaggaatgltatitgttggltgtttctcgtgggtgaactggtttcaaatgltac	981
Db	721	GAGTTACGGGGAGATGATGTATGTGGGTGTTTCTCTGGGGTCACGTGTTCAAAATGTTAC	780
OY	982	agaagaaagcctaataatacatgtcttcagcccttgcagatcccacagaagtgltatg	1041
Db	781	AGAAGAAAAGCGCTAAATATCATTTGCTTCAGCCCTTGCCAGATCCACAGAAAGTGTTATG	840
OY	1042	gagttaaaagaaaaaacatccatcttagagacaaatactgcgtgtatgtatgtat	1100
Db	841	GAGGTACAAAGGAAAAAACATCCACATTAGAGCAATATCGGCTGTATGATTGGAT	900
OY	1102	accocgaatgatcttcttgtcatcccaaaacaaagcttttaactcaatggttggat	1161
Db	901	ACCCCAAGATATGATTTTGGTGTATCCCAAAACCAAGCTTTTATCTACTCATGTGGAT	960
OY	1162	gaatggagatcatalgaactctatccatctgggtgccctatgctggagagttcccatattgg	1221
Db	961	GAATGGGATGTATGAACCTATTACCATGGGGTCCCTATGTGGGATTTCCCATATTGG	1020
OY	1222	tgatcagcttgataaacaatagctccatgaagccaaaggagcagctgtagaataaact	1281
Db	1021	TGATCAGCTTGATTAACATTAACCTCACATGAAGGCCAAAGAGCAGCTGTAGAAATTAACCT	1080
OY	1282	caaaactaibaacaagcgaagaatttactctggggcttggaaacagatcaacgattctc	1341
Db	1081	CAAAACTATGACAAAGCCAAATATTACTGAAGGCTTTGAABAACAGTCATTAACGATTCTC	1140
OY	1342	ttataagagaatibctaigtatatacaagaatticaaccatgtaacactgtaaagccct	1401
Db	1141	TTATTAAGAGAAATGCTATGAGATTATCAAGAAATTCACATGATCAACCTGTAAAGCCCT	1200
OY	1402	agatcagcagctctctctgagctgagttgtcatgcbgcacaaaggagcccaagcactgcg	1461
Db	1201	AGATCGAGCAGATCTTTCGTGATCGAGTTGTTCATAGCCGCCCAAGAGAGCCAAACACTCTCG	1260
OY	1462	atcagctggccatbaacttaacactcgtgttccaagcaactctataagatgtgattggttct	1521
Db	1261	ATCAGCTGCCCATATCCTCACTCGTGTTCAGCACTATCTATAGAGTGTGATTTGGTCTCT	1320
OY	1522	gctacactgtgtggcaactctctatctctgtgtcacaaaatlttttatttctcgtgca	1581
Db	1321	GCTGGCCGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTATTTTCTGTCCA	1380
OY	1582	aaaaatttaataaaaactagaaagatagaaaagggaatagatcttccaatitcaagaa	1641
Db	1381	AAAATTTAAATTAACCTAGAAAGATAGAAAAGAGGAAATGATCTTTCCAAATTCAGAAA	1440
OY	1642	gaacttgatgggtatctcttctaattccagccaatagaaatttggtaaaacactgcat	1700
Db	1441	GACCTGATGGGGTAAATCTCTGTAAATTCAGGCCACATAGAAATTTGGTGAACCTTGCTAT	1500
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OY	1822	ctcaacttggacaacagagacatgaataaactcaaatcttctcatatttctgatatcaact	1881
Db	1621	CTCACCTTTGTACCAAGGACATGAATACATCTTAAATTTTCCATATTCTGATATATACGT	1680

QY	1882	tccatgaagctaatctacttctctaaccctaaagtacgataagggtgcacctcgcgaatatgctgatt	1941
Db	1681	TTTTGATGGATGTCAATTACTTCTAATAACCTTAAGGAATAGGGTGACATGCACAATATGATTTATTT	1740
QY	1942	cctgcttgtttcacaacaacatcgatgctgtaagaagtaaaaatgtaaaattcacaaant	2001
Db	1741	CCTGGTGTCCGCCCANACCATGGATATATAAGGGRRAAAACTTAATAATTCCAAAAATT	1800
QY	2002	cagtaaaccacaacaatacaatgaagcatctatgaacattagctgltatgtagtaacataa	2061
Db	1801	CAGTAACACACAAATCAGGTAGAGTGTCTATAGAGTTTAGTGGCGTATGAGAAGAACATTA	1860
QY	2062	tgactttcttcttccaattaaataaagcccttcacatcccagcatctactgatctaga	2121
Db	1861	TGATGTTTTCTTTTCATTTAAATTAATAGACCCTTCTACATACCCGACATCACTGATCTCGA	1920
QY	2122	caatgaattggctaaaaaabaagcaiaaggagattacacacacagaaatagtttgttatctca	2181
Db	1921	AAATAAATTTGCTPAATATATATGACATGAGCAATVATMGCTTACAAAAGTTTGCTGTAATTTCCA	1980
QY	2182	cataccatcatcagaatgcatagcaccatcttctgcacatcaactuaactgaca-cttttgg	2240
Db	1981	TGACCTCATCTAGATNGTGTATGSCCTACATTTCTGCCATACACACCAATACTTTTTC	2040
QY	2241	tgtgtcttgatgataaataagacagttcttatattatgcttcacaataataaagaacag	2300
Db	2041	TGTTTTCTTGANGATATAAAAAGACCTTTCATGATGATGCCATCAAAATPACAAAAGAACTA	2100
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QY	2419	tgttacactt-----gattlaaatgltctattctt-aaaaatgatgaatacctaatactc	2471
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QY	2472	ttatctctaatcaaaagtataatttaccgtctgagaaaaataaagagatgctgttctcgaa	2531
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QY	2532	agtaaa 2538 	
Db	2340	AGTAAGA 2346	
RESULT	2		
AF175221	2547 bp	mRNA	ROD 29-AUG-1999
LOCUS	AF175221	Cavia porcellus UDP glucuronosyltransferase UGT2A3 mRNA, complete cds.	
DEFINITION	AF175221	GI:5802603	
ACCESSION	AF175221.1		
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
		domestic guinea pig. Cavia porcellus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia. 1 (bases 1 to 2547) Smith,S.A., Nagalla,S.R., Andrews,D.P. and Olsen,G.D. Morphine regulation of a novel uridine diphosphate glucuronosyltransferase in guinea pig pups following in utero exposure	
JOURNAL	MOL. Genet. Metab. (1999) In press		
REFERENCE	2 (bases 1 to 2547)		
AUTHORS	Smith,S.A., Nagalla,S.R., Andrews,D.P. and Olsen,G.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-AUG-1999) Pediatrics, Oregon Health Sciences University, 3181 SW Sam Jackson Park Road, Portland, OR 97201, USA		
FEATURES	Location/Qualifiers		

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20. .1612
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VTKCLFSPNFRIKIGRIKKE"
BASE COUNT      765 a      469 c      523 g      790 t
ORIGIN

Query Match      37.7%   Score 1038.8; DB 94; Length 2547;
Best Local Similarity 76.0%   Pred. No. 1.2e-175;
Matches 1299; Conservative 0; Mismatches 402; Indels 9; Gaps 1;

26 ggaactgcacatgaagtcctgaagaagtcagcttctgtattctgtcctgcagctcttc 85
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   8 GGAAGGCGCAGATGGCTCTGGAGAGTGGCTTCGACAGTCTGCTGCTGCTCTGCG 67

86 tctgttgcttgatctctgttggaagtcctgtgtgttgccctgtgacatgaagcatgg 145
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   68 TGTGCGCGCTGTGATCTTCTGTGGAGAGGTGCTGTGCTGCGGTGAATGAGCCACTGG 127

146 cthaatgtaagtlcatagaagaagtcataagtgagagccatgaagtaagtaagtttg 205
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   128 CTCATTAATTAAGACTCTCTGTGAGAGCTTGTAAGAAAGAGACATGAGGTGAGTTCG 187

206 actcaatcaagaagcttcgttaattgaatgaagaagccttcgtcattgaatttgagtg 265
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   188 ACTCTTTAAACACTTTGTTATTGACTACCAACAGACATCTCTTTAATTTTGAAGTG 247

266 gtccatatcccaagcaagaagaagaatgaata-----tttgtgaaccta 316
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   248 ATGCCGTGACCAACTGACAAAACATGCTGAGAAATATATCTAATAGTTTATAGAACTA 307

317 gctctgaatgtcttgccaggtctatcaacctggaacagttataaataatgaatttt 376
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   308 GGTGTGAATGTATGCCAACAAATGCTCTGTGCAATCAGGAAACTACTGCAACAAATTC 367

377 ttgtgtaataaggaagcaatttaaaatgagtgtgagaagctttctacaatcagaag 436
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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AUTHORS	Lal, P., Yue, H., Tang, Y. T., Hillman, J. L., Baughn, M. R. and Yang, J.		
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Levesque,E., Beaulieu,M., Green,M.D., Tephly,T.R., Belanger,A. and Hum,D.W.				
TITLE	Isolation and characterization of UGT2B15(Y85): a UDP-glucuronosyltransferase encoded by a polymorphic gene				
JOURNAL	Pharmacogenetics 7 (4), 317-325 (1997)				
MEDLINE	97439504				
REFERENCE	2 (bases 1 to 2114)				
AUTHORS	Levesque,E., Beaulieu,M., Green,M.D., Tephly,T.R., Belanger,A. and Hum,D.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (24-AUG-1999) Molecular Endocrinology, CHU Research Center, 2705 Laurier Blvd, Ste-Foy, Quebec G1V 4G2, Canada				
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 REFERENCE 1 (bases 1 to 2107)
 AUTHORS Beaulieu, M., Levesque, E., Hum, D.W. and Belanger, A.
 TITLE Isolation and characterization of a novel cDNA encoding a human UDP-glucuronosyltransferase active on C19 steroids
 JOURNAL J. Biol. Chem. 271 (37), 22855-22862 (1996)
 JOURNAL MEDLINE 96394358
 REFERENCE 2 (bases 1 to 2107)
 AUTHORS Hum, D.W., Belanger, A., Beaulieu, M. and Levesque, E.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAY-1996) Laboratory of Molecular Endocrinology, Centre Hospitalier de l'universite Laval, 2705 Boul. Laurier, Ste-Foy, Quebec G1V 4G2, Canada
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		Belanger,G., Barbier,O., Hum,D.W. and Belanger,A.	
		Molecular cloning, expression and characterization of a monkey	
		steroid UDP-glucuronosyltransferase, UGT2B19, that conjugates	
		testosterone	
		Eur. J. Biochem. 260 (3), 701-708 (1999)	
		99203465	
		2 (bases 1 to 2108)	
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		Direct Submission	
		Submitted (07-DEC-1998) Molecular Endocrinology, CHUL Research	
		Center, 2705 Laurier Blvd, Sainte Foy, Quebec G1V 4G2, Canada	
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DEFINITION Homo sapiens mRNA for UDP-glucuronosyltransferase.
ACCESSION AJ005162
VERSION AJ005162.1 GI:3135024
KEYWORDS UDP-glucuronosyltransferase; UGT2B4 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2079)
AUTHORS Rittler,J.K.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-1998) Rittler J.K., Pharmacology and Toxicology,
Virginia Commonwealth University, P.O. Box 980613, Medical College
of Virginia, Richmond, Virginia, 23112-0613, USA
2 (bases 1 to 2079)
AUTHORS Rittler,J.K., Chen,F., Sheen,Y.Y., Lubet,R.A. and Owens,I.S.
TITLE Two human liver cDNAs encode UDP-glucuronosyltransferases with 2
log differences in activity toward parallel substrates including
hydroxycholeic acid and certain estrogen derivatives
JOURNAL Biochemistry 31 (13), 3409-3414 (1992)
MEDLINE 92207964
REFERENCE 3 (bases 1 to 2079)
AUTHORS Jackson,M.R., McCarthy,L.R., Harding,D., Wilson,S., Coughtrie,M.W.
and Burchell,B.
TITLE Cloning of a human liver microsomal UDP-glucuronosyltransferase
cDNA
JOURNAL Biochem. J. 242 (2), 581-588 (1987)
MEDLINE 87241362
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ACCESSION	Homo sapiens UDP-glucuronosyltransferase 2B4
VERSION	mRNA, UG12B4*E458 allele, complete cds.
KEYWORDS	AF064200.1 GI:3153831
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 2097)
LEVESQUE, E., BEAULIEU, M., HUM, M. and BELANGER, A.	Characterization and substrate specificity of UGT2B4 (E458) : A UDP-glucuronosyltransferase encoded by a polymorphic gene
Pharmacogenetics (1999)	In press
2 (bases 1 to 2097)	
LEVESQUE, E., BEAULIEU, M. and BELANGER, A.	Direct Submission
JOURNAL	Submitted (08-MAY-1999)
REFERENCE	Molecular Endocrinology, CHUL Research
AUTHORS	Center, 2705 Laurier Blvd, Ste-Foy, PQ G1V 4G2, Canada
TITLE	Location/Qualifiers
JOURNAL	1. 2097
FEATURES	
source	

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ACCESSION	AF081793		
VERSION	AF081793.1		
KEYWORDS	GI:3426331		
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 2091)		
JOURNAL	Jin,C.J., Milners,J.O., Lillywhite,K.J. and Mackenzie,P.I.		
MEDLINE	cDNA cloning and expression of two new members of the human liver		
REFERENCE	UDP-glucuronosyltransferase 2B subfamily		
AUTHORS	Biochem. Biophys. Res. Commun. 194 (1), 496-503 (1993)		
TITLE	2 (bases 1 to 2091)		
JOURNAL	Mackenzie,P.I.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (30-JUL-1998) Clinical Pharmacology, Flinders University		
TITLE	of South Australia, Bedford Park, SA 5042, Australia		
JOURNAL	Location/Qualifiers		
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